Conclusions :

   In the past, scientists could only analyze a limited part of the human genome because of its length. Recently, microarrays have emerged to fundamentally change this type of research. Today, scientists perform microarray or high-throughput sequencing experiments to generate the entire genome profile, then they can mine information from any regions in it.

   It is preferred to upload the data to clementine in spss file rather than excel sheet because clementine can read excel sheet in xls extension only and the size of this extension is not more than 256 columns .

   Neural network and PCA models in clementine can not executed with a huge number of data so it is preferred to reduce the number of data by executing feature selection model firstly .

Recommendations:

   It is recommended to use different model rather than the neural network and PCA for the classifying of the data. Clementine provides wide range of predictive algorithms.

   It is also recommended to use the result of this project to build a tool that may help the diabetic patients to predict the probability of infection of diabetic patient with heart diseases .

   We also recommend applying this project analysis on Sudanese micro-array data sets so as to help illuminating the challenges that faces Sudanese in diagnosing and treating this disease. Collaboration between researchers in computer science, veterinary and medical fields would play a major role in the goal of our project .